

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/573,130B
Source: 1FWP
Date Processed by STIC: 12/1/06

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RAW SEQUENCE LISTING

DATE: 12/01/2006

PATENT APPLICATION: US/10/573,130B

TIME: 14:16:00

Input Set : A:\Replacement Sequence List-13111-00035-US.txt

Output Set: N:\CRF4\12012006\J573130B.raw

```

3 <110> APPLICANT: Sturmer, Rainer
4     Kessler, Maria
5     Hauer, Bernhard
6     Friedrich, Thomas
7     Breuer, Michael
9 <120> TITLE OF INVENTION: Methods for the production of
10    3-methylamino-1-(thiene-2-yl)-propane-1-ol
12 <130> FILE REFERENCE: 13111-00035-US
14 <140> CURRENT APPLICATION NUMBER: US/10/573,130B
15 <141> CURRENT FILING DATE: 2006-03-23
17 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/010939
18 <151> PRIOR FILING DATE: 2004-09-30
20 <150> PRIOR APPLICATION NUMBER: DE 103 45 772.0
21 <151> PRIOR FILING DATE: 2003-10-01
23 <160> NUMBER OF SEQ ID NOS: 44
25 <170> SOFTWARE: PatentIn version 3.3
28 <210> SEQ ID NO: 1
30 <211> LENGTH: 47
32 <212> TYPE: PRT
34 <213> ORGANISM: Lactobacillus brevis
37 <400> SEQUENCE: 1
39 Met Ser Asn Arg Leu Asp Gly Lys Val Ala Ile Val Thr Gly Gly Thr
40 1          5          10          15
43 Leu Gly Ile Gly Leu Ala Ile Ala Thr Lys Phe Val Glu Glu Gly Ala
44          20          25          30
47 Lys Val Met Ile Thr Gly Arg His Ser Asp Val Gly Glu Lys Ala
48          35          40          45
51 <210> SEQ ID NO: 2
53 <211> LENGTH: 18
55 <212> TYPE: PRT
57 <213> ORGANISM: Candida magnoliae
60 <400> SEQUENCE: 2
62 Ser Asn Ala Leu Val Thr Gly Gly Ser Arg Val Ile Gly Ala Gly Gly
63 1          5          10          15
66 Phe Ile
70 <210> SEQ ID NO: 3
72 <211> LENGTH: 756
74 <212> TYPE: DNA
76 <213> ORGANISM: Lactobacillus brevis
79 <220> FEATURE:
81 <221> NAME/KEY: CDS
83 <222> LOCATION: (1)..(756)
86 <400> SEQUENCE: 3

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87 atg tct aac cgt ttg gat gga aaa gta gca atc gtt aca ggt ggt acg      48
88 Met Ser Asn Arg Leu Asp Gly Lys Val Ala Ile Val Thr Gly Gly Thr
89 1          5          10          15
91 ttg ggt atc ggt tta gct atc gcc acg aag ttc gtt gaa gaa ggg gct      96
92 Leu Gly Ile Gly Leu Ala Ile Ala Thr Lys Phe Val Glu Glu Gly Ala
93          20          25          30
95 aag gtc atg att acc ggc cgg cac agc gat gtt ggt gaa aaa gca gct      144
96 Lys Val Met Ile Thr Gly Arg His Ser Asp Val Gly Glu Lys Ala Ala
97          35          40          45
99 aag agt gtc ggc act cct gat cag att caa ttt ttc caa cat gat tct      192
100 Lys Ser Val Gly Thr Pro Asp Gln Ile Gln Phe Phe Gln His Asp Ser
101          50          55          60
103 tcc gat gaa gac ggc tgg acg aaa tta ttc gat gca acg gaa aaa gcc      240
104 Ser Asp Glu Asp Gly Trp Thr Lys Leu Phe Asp Ala Thr Glu Lys Ala
105 65          70          75          80
107 ttt ggc cca gtt tct aca tta gtt aat aac gct ggg atc gcg gtt aac      288
108 Phe Gly Pro Val Ser Thr Leu Val Asn Asn Ala Gly Ile Ala Val Asn
109          85          90          95
111 aag agt gtc gaa gaa acc acg act gct gaa tgg cgt aaa cta tta gcc      336
112 Lys Ser Val Glu Thr Thr Thr Ala Glu Trp Arg Lys Leu Leu Ala
113          100          105          110
115 gtc aac ctt gat ggt gtc ttc ttc ggt acc cga tta ggg att caa cgg      384
116 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
117          115          120          125
119 atg aag aac aaa ggc tta ggg gct tcc atc atc aac atg tct tcg atc      432
120 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
121          130          135          140
123 gaa ggc ttt gtg ggt gat cct agc tta ggg gct tac aac gca tct aaa      480
124 Glu Gly Phe Val Gly Asp Pro Ser Leu Gly Ala Tyr Asn Ala Ser Lys
125 145          150          155          160
127 ggg gcc gta cgg att atg tcc aag tca gct gcc tta gat tgt gcc cta      528
128 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
129          165          170          175
131 aag gac tac gat gtt cgg gta aac act gtt cac cct ggc tac atc aag      576
132 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Tyr Ile Lys
133          180          185          190
135 aca cca ttg gtt gat gac cta cca ggg gcc gaa gaa gcg atg tca caa      624
136 Thr Pro Leu Val Asp Asp Leu Pro Gly Ala Glu Glu Ala Met Ser Gln
137          195          200          205
139 cgg acc aag acg cca atg ggc cat atc ggt gaa cct aac gat att gcc      672
140 Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
141          210          215          220
143 tac atc tgt gtt tac ttg gct tct aac gaa tct aaa ttt gca acg ggt      720
144 Tyr Ile Cys Val Tyr Leu Ala Ser Asn Glu Ser Lys Phe Ala Thr Gly
145 225          230          235          240
147 tct gaa ttt gta gtt gac ggt ggc tac act gct caa      756
148 Ser Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
149          245          250
152 <210> SEQ ID NO: 4

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Input Set : A:\Replacement Sequence List-13111-00035-US.txt

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154 <211> LENGTH: 252

156 <212> TYPE: PRT

158 <213> ORGANISM: Lactobacillus brevis

161 <400> SEQUENCE: 4

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163 Met Ser Asn Arg Leu Asp Gly Lys Val Ala Ile Val Thr Gly Gly Thr
164 1 5 10 15
167 Leu Gly Ile Gly Leu Ala Ile Ala Thr Lys Phe Val Glu Glu Gly Ala
168 20 25 30
171 Lys Val Met Ile Thr Gly Arg His Ser Asp Val Gly Glu Lys Ala Ala
172 35 40 45
175 Lys Ser Val Gly Thr Pro Asp Gln Ile Gln Phe Phe Gln His Asp Ser
176 50 55 60
179 Ser Asp Glu Asp Gly Trp Thr Lys Leu Phe Asp Ala Thr Glu Lys Ala
180 65 70 75 80
183 Phe Gly Pro Val Ser Thr Leu Val Asn Asn Ala Gly Ile Ala Val Asn
184 85 90 95
187 Lys Ser Val Glu Glu Thr Thr Thr Ala Glu Trp Arg Lys Leu Leu Ala
188 100 105 110
191 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
192 115 120 125
195 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
196 130 135 140
199 Glu Gly Phe Val Gly Asp Pro Ser Leu Gly Ala Tyr Asn Ala Ser Lys
200 145 150 155 160
203 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
204 165 170 175
207 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Tyr Ile Lys
208 180 185 190
211 Thr Pro Leu Val Asp Asp Leu Pro Gly Ala Glu Glu Ala Met Ser Gln
212 195 200 205
215 Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
216 210 215 220
219 Tyr Ile Cys Val Tyr Leu Ala Ser Asn Glu Ser Lys Phe Ala Thr Gly
220 225 230 235 240
223 Ser Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
224 245 250

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227 <210> SEQ ID NO: 5

229 <211> LENGTH: 472

231 <212> TYPE: DNA

233 <213> ORGANISM: Candida magnoliae

236 <220> FEATURE:

238 <221> NAME/KEY: CDS

240 <222> LOCATION: (1)..(471)

243 <400> SEQUENCE: 5

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244 aac gcg ctg gtg acg ggc ggc agc cgc ggc att ggc gaa gcc act gcc 48
245 Asn Ala Leu Val Thr Gly Gly Ser Arg Gly Ile Gly Glu Ala Thr Ala
246 1 5 10 15
248 att aag ctc gcc gag gag ggc tac agc gtc acg att gcg tct cgc ggc 96
249 Ile Lys Leu Ala Glu Glu Gly Tyr Ser Val Thr Ile Ala Ser Arg Gly

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250          20          25          30
252 ctt aag cag ctc gag gct gtg aag gcc aaa cta ccc att gtg aag cag      144
253 Leu Lys Gln Leu Glu Ala Val Lys Ala Lys Leu Pro Ile Val Lys Gln
254          35          40          45
256 gga cag gtt cac cac gtg tgg cag ctt gat ctc agt gat gtc gac gct      192
257 Gly Gln Val His His Val Trp Gln Leu Asp Leu Ser Asp Val Asp Ala
258          50          55          60
260 gcg gcc gcc ttc aaa ggg tgc ccg cta cct gcc agc cgc tac gac gtg      240
261 Ala Ala Ala Phe Lys Gly Ser Pro Leu Pro Ala Ser Arg Tyr Asp Val
262 65          70          75          80
264 ctc gtc agc aat gct ggc gtg gcc cag ttt agc ccg ttc atc gag cat      288
265 Leu Val Ser Asn Ala Gly Val Ala Gln Phe Ser Pro Phe Ile Glu His
266          85          90          95
268 gcg aag cag gac tgg tgc cag atg ctt gcc atc aat ctg gcg gca ccc      336
269 Ala Lys Gln Asp Trp Ser Gln Met Leu Ala Ile Asn Leu Ala Ala Pro
270          100          105          110
272 att gcg ctg gcc cag aca ttt gct aag gcc att ggc gac aag ccg cgc      384
273 Ile Ala Leu Ala Gln Thr Phe Ala Lys Ala Ile Gly Asp Lys Pro Arg
274          115          120          125
276 aac aca ccg gcc cac att gtg ttt gtc tgc tgc aac gtc tgc ttg cga      432
277 Asn Thr Pro Ala His Ile Val Phe Val Ser Ser Asn Val Ser Leu Arg
278          130          135          140
280 ggc ttc ccg aac atc ggc gtc aac tcc atc acc ccc ggc a      472
281 Gly Phe Pro Asn Ile Gly Val Asn Ser Ile Thr Pro Gly
282 145          150          155
285 <210> SEQ ID NO: 6
287 <211> LENGTH: 157
289 <212> TYPE: PRT
291 <213> ORGANISM: Candida magnoliae
294 <400> SEQUENCE: 6
296 Asn Ala Leu Val Thr Gly Gly Ser Arg Gly Ile Gly Glu Ala Thr Ala
297 1          5          10          15
300 Ile Lys Leu Ala Glu Glu Gly Tyr Ser Val Thr Ile Ala Ser Arg Gly
301          20          25          30
304 Leu Lys Gln Leu Glu Ala Val Lys Ala Lys Leu Pro Ile Val Lys Gln
305          35          40          45
308 Gly Gln Val His His Val Trp Gln Leu Asp Leu Ser Asp Val Asp Ala
309          50          55          60
312 Ala Ala Ala Phe Lys Gly Ser Pro Leu Pro Ala Ser Arg Tyr Asp Val
313 65          70          75          80
316 Leu Val Ser Asn Ala Gly Val Ala Gln Phe Ser Pro Phe Ile Glu His
317          85          90          95
320 Ala Lys Gln Asp Trp Ser Gln Met Leu Ala Ile Asn Leu Ala Ala Pro
321          100          105          110
324 Ile Ala Leu Ala Gln Thr Phe Ala Lys Ala Ile Gly Asp Lys Pro Arg
325          115          120          125
328 Asn Thr Pro Ala His Ile Val Phe Val Ser Ser Asn Val Ser Leu Arg
329          130          135          140
332 Gly Phe Pro Asn Ile Gly Val Asn Ser Ile Thr Pro Gly

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Input Set : A:\Replacement Sequence List-13111-00035-US.txt

Output Set: N:\CRF4\12012006\J573130B.raw

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333 145          150          155
337 <210> SEQ ID NO: 7
338 <211> LENGTH: 27
339 <212> TYPE: DNA
340 <213> ORGANISM: Artificial sequence
342 <220> FEATURE:
343 <223> OTHER INFORMATION: Primer: Mke 338
345 <400> SEQUENCE: 7
346 gggaattcca tatgtctaac cgtttgg                27
349 <210> SEQ ID NO: 8
350 <211> LENGTH: 28
351 <212> TYPE: DNA
352 <213> ORGANISM: Artificial sequence
354 <220> FEATURE:
355 <223> OTHER INFORMATION: Primer: Mke 339
357 <400> SEQUENCE: 8
358 cgtagggaag cttattgagc agtgtagc                28
361 <210> SEQ ID NO: 9
362 <211> LENGTH: 28
363 <212> TYPE: DNA
364 <213> ORGANISM: Artificial sequence
366 <220> FEATURE:
367 <223> OTHER INFORMATION: Primer: Mke 366
369 <400> SEQUENCE: 9
370 acgacgacga gcaacgcbct bgtbacgg                28
373 <210> SEQ ID NO: 10
374 <211> LENGTH: 28
375 <212> TYPE: DNA
376 <213> ORGANISM: Artificial sequence
378 <220> FEATURE:
379 <223> OTHER INFORMATION: Primer: Mke 367
381 <400> SEQUENCE: 10
382 acgacgacgt cgaacgcbct bgtbacgg                28
385 <210> SEQ ID NO: 11
386 <211> LENGTH: 27
387 <212> TYPE: DNA
388 <213> ORGANISM: Artificial sequence
390 <220> FEATURE:
391 <223> OTHER INFORMATION: Primer: Mke 374
393 <400> SEQUENCE: 11
394 gccgggggttg atsswggttsa cgccgat                27
397 <210> SEQ ID NO: 12
398 <211> LENGTH: 10
399 <212> TYPE: PRT
400 <213> ORGANISM: Lactobacillus brevis
403 <220> FEATURE:
404 <221> NAME/KEY: MISC_FEATURE
405 <222> LOCATION: (1)..(10)
406 <223> OTHER INFORMATION: Fragment: C terminus

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/573,130B

DATE: 12/01/2006
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Input Set : A:\Replacement Sequence List-13111-00035-US.txt
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FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:15; Xaa Pos. 47,48,53,59,60
 Seq#:16; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,19,20
 Seq#:17; Xaa Pos. 12,13,14,15
 Seq#:18; Xaa Pos. 8
 Seq#:19; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15
 Seq#:20; Xaa Pos. 1,2,3,4
 Seq#:21; Xaa Pos. 1,2,4,5,7
 Seq#:22; Xaa Pos. 6,10,11,12,13,14,15
 Seq#:23; Xaa Pos. 1,3,4,5,6,7,8,9,11,12,13,14,15,16,17,18
 Seq#:24; Xaa Pos. 6,10,11,12,13,14,15,16,17
 Seq#:25; Xaa Pos. 16,17,18,19,20
 Seq#:26; Xaa Pos. 1,3
 Seq#:27; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15
 Seq#:28; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20
 Seq#:29; Xaa Pos. 1,2,3,4,5,7,8,9,10,11,12,13,15,16,17,18,19,20,21,23,24
 Seq#:30; Xaa Pos. 1,2,5,10,11,12,13,14,15,16,17,18,19,20
 Seq#:31; Xaa Pos. 1,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19
 Seq#:32; Xaa Pos. 1,2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,29,30
 Seq#:33; Xaa Pos. 5,6,7,8,9,10
 Seq#:34; Xaa Pos. 1,2,3,4,5,6,8,9,13,14,15,16,17,18,19,20
 Seq#:35; Xaa Pos. 11,12,13,14
 Seq#:36; Xaa Pos. 1,2,24,30
 Seq#:39; Xaa Pos. 1,3,5,6,7,8
 Seq#:40; Xaa Pos. 1,2,3,4,5,14,15,19,20,22
 Seq#:41; Xaa Pos. 2,39,40
 Seq#:42; Xaa Pos. 3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,25,27
 Seq#:42; Xaa Pos. 37,38,39
 Seq#:43; Xaa Pos. 12,13,14,15
 Seq#:44; Xaa Pos. 1,4,5,6,7,8,9,11,12,13,14,15

VERIFICATION SUMMARY

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Input Set : A:\Replacement Sequence List-13111-00035-US.txt

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L:492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:32
L:496 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:48
L:592 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:596 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:16
L:617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:634 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:705 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:737 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:775 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:801 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:898 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0
L:902 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:16
L:924 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
L:928 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:16
L:945 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:949 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:16
L:971 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:1058 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
L:1155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
L:1159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:16
L:1280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
L:1284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:16
L:1321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:1325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:16
L:1431 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:1435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:16
L:1551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:1555 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:16
L:1572 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:1633 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
L:1637 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:16
L:1654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0
L:1686 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0
L:1690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:16
L:1754 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0
L:1816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0
L:1820 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:16
L:1846 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:0
L:1854 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:32
L:1980 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0
L:1984 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:16
L:1988 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:32
L:2005 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0
L:2067 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0